SF2001-014-2US

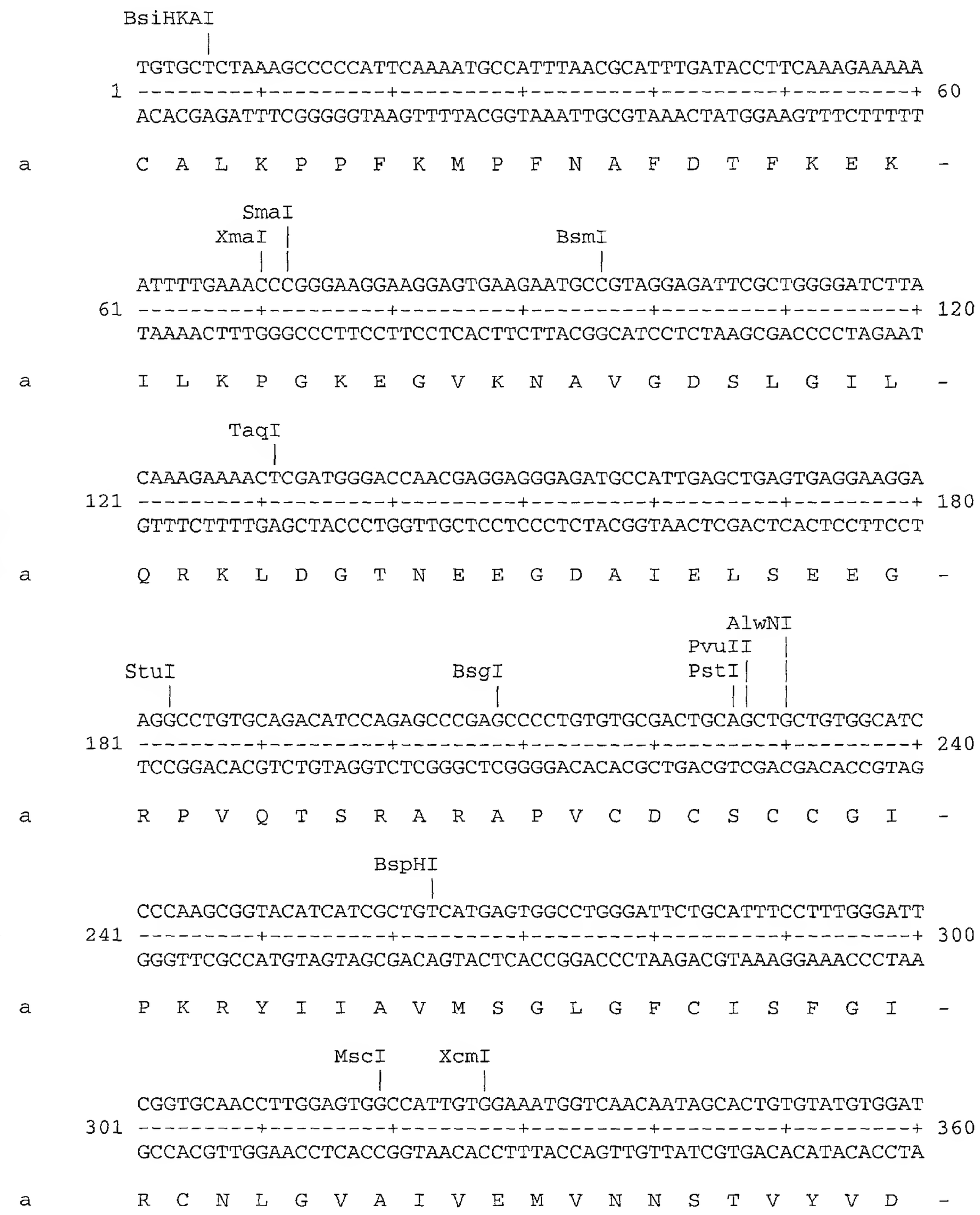

Fig. 1

```
                                               BsmBI
       BsaWI                                 BamHI| BmrI              EcoRI
           |                                      ||    |                 |
       GGGAAACCGGAAATCCAGACAGCACAGTTTAACTGGGATCCAGAGACGGTGGGAAGGGCG
   361 ---------+---------+---------+---------+---------+---------+ 420
       CCCTTTGGCCTTTAGGTCTGTCGTGTCAAATTGACCCTAGGTCTCTGCCACCCTTCCCGC

a      G  K  P  E  I  Q  T  A  Q  F  N  W  D  P  E  T  V  G  R  A   -

                                                MaeIII
                  NcoI                          Tsp45I
                     |                               |
       AATTCTCTTATCCATGGATCTTTTTTCTGGGGTTATATTGTGACACAAATTCCCGGTGGC
   421 ---------+---------+---------+---------+---------+---------+ 480
       TTAAGAGAATAGGTACCTAGAAAAAAGACCCCAATATAACACTGTGTTTAAGGGCCACCG

a      N  S  L  I  H  G  S  F  F  W  G  Y  I  V  T  Q  I  P  G  G   -

                                                                AatII
                                                           BsaHI    |
                                                               |    |
       TTCATTTCAAACAAGTTTGCTGCTAACAGGGTCTTTGGAGCTGCCATCTTCTTGACGTCA
   481 ---------+---------+---------+---------+---------+---------+ 540
       AAGTAAAGTTTGTTCAAACGACGATTGTCCCAGAAACCTCGACGGTAGAAGAACTGCAGT

a      F  I  S  N  K  F  A  A  N  R  V  F  G  A  A  I  F  L  T  S   -

             XmnI            SacII
          PciI |           BstUI|
             | |               ||
       ACCCTGAACATGTTCATCCCTTCCGCGGCCAGGGTGCATTACGGCTGTGTCATGTGTGTG
   541 ---------+---------+---------+---------+---------+---------+ 600
       TGGGACTTGTACAAGTAGGGAAGGCGCCGGTCCCACGTAATGCCGACACAGTACACACAC

a      T  L  N  M  F  I  P  S  A  A  R  V  H  Y  G  C  V  M  C  V   -

                             MaeIII
                  AlwNI      Tsp45I
                      |           |
       AGGATTTTGCAGGGTCTGGTGGAGGGTGTGACCTACCCAGCCTGCCACGGGATGTGGAGT
   601 ---------+---------+---------+---------+---------+---------+ 660
       TCCTAAAACGTCCCAGACCACCTCCCACACTGGATGGGTCGGACGGTGCCCTACACCTCA

a      R  I  L  Q  G  L  V  E  G  V  T  Y  P  A  C  H  G  M  W  S   -
                                           BpmI
                                              |
       AAGTGGGCACCTCCCCTGGAGAGAAGTCGTCTAGCCACAACCTCTTTTTGTGGTTCCTAT
   661 ---------+---------+---------+---------+---------+---------+ 720
       TTCACCCGTGGAGGGGACCTCTCTTCAGCAGATCGGTGTTGGAGAAAAACACCAAGGATA

a      K  W  A  P  P  L  E  R  S  R  L  A  T  T  S  F  C  G  S  Y   -
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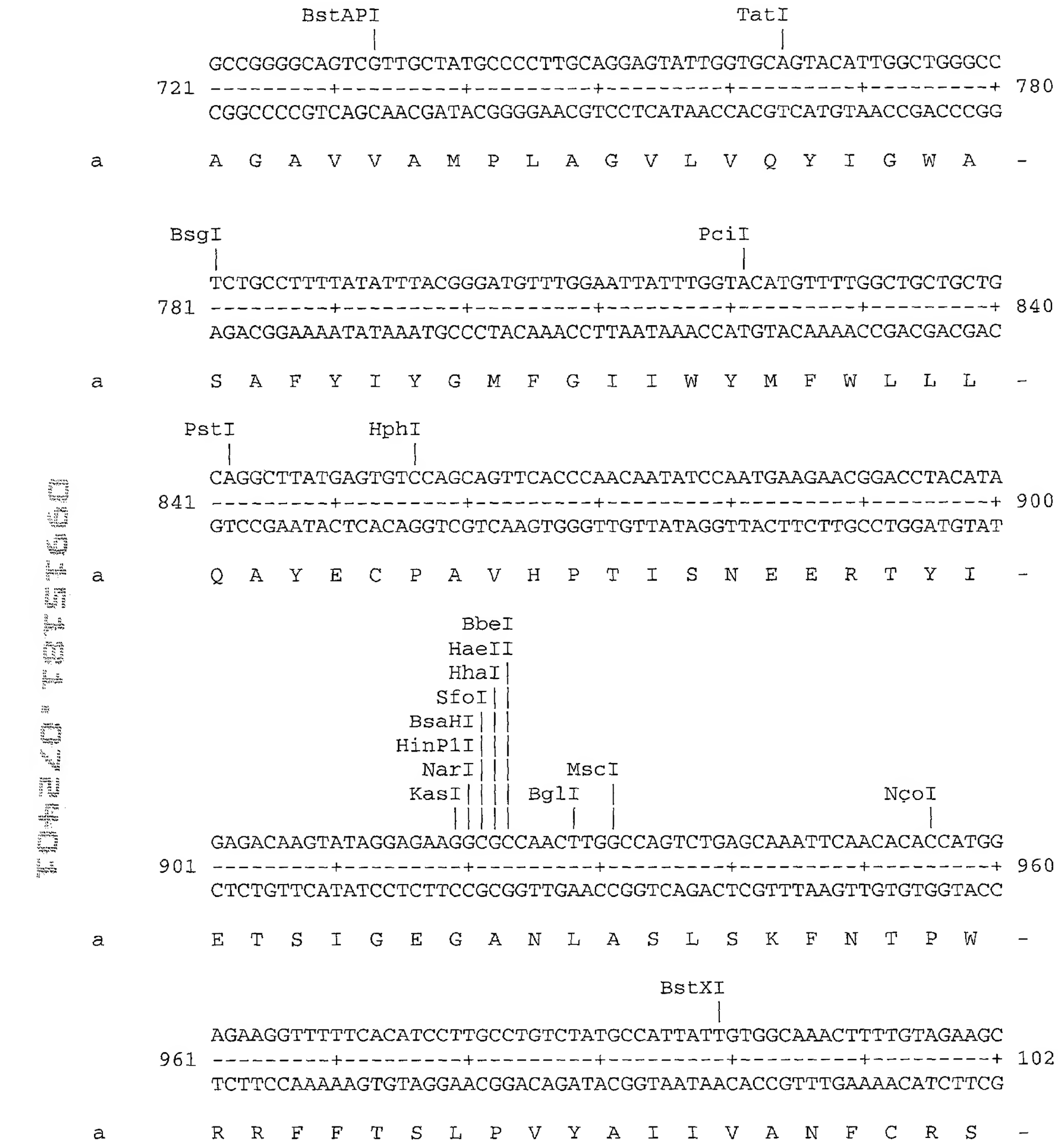
Fig. 1 cont'd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721 ---------+---------+---------+---------+---------+---------+---------+ 780
CGGCCCCGTCAGCAACGATACGGGGAACGTCCTCATAACCACGTCATGTAACCGACCCGG
a A G A V V A M P L A G V L V Q Y I G W A -
BsgI
PciI
TCTGCCTTTTATATTTACGGGATGTTTGGAATTATTTGGTACATGTTTTGGCTGCTGCTG
781 ---------+---------+---------+---------+---------+---------+---------+ 840
AGACGGAAAATATAAATGCCCTACAAACCTTAATAAACCATGTACAAAACCGACGACGAC
a S A F Y I Y G M F G I I W Y M F W L L L -
PstI
HphI
CAGGCTTATGAGTGTCCAGCAGTTCACCCAACAATATCCAATGAAGAACGGACCTACATA
841 ---------+---------+---------+---------+---------+---------+---------+ 900
GTCCGAATACTCACAGGTCGTCAAGTGGGTTGTTATAGGTTACTTCTTGCCTGGATGTAT
a Q A Y E C P A V H P T I S N E E R T Y I -
BbeI
HaeII
HhaI
SfoI
BsaHI
HinP1I
NarI
MscI
KasI
BglI
NçoI
GAGACAAGTATAGGAGAAGGCGCCAACTTGGCCAGTCTGAGCAAATTCAACACACCATGG
901 ---------+---------+---------+---------+---------+---------+---------+ 960
CTCTGTTCATATCCTCTTCCGCGGTTGAACCGGTCAGACTCGTTTAAGTTGTGTGGTACC
a E T S I G E G A N L A S L S K F N T P W -
BstXI
AGAAGGTTTTTCACATCCTTGCCTGTCTATGCCATTATTGTGGCAAACTTTTGTAGAAGC
961 ---------+---------+---------+---------+---------+---------+---------+ 1020
TCTTCCAAAAAGTGTAGGAACGGACAGATACGGTAATAACACCGTTTGAAAACATCTTCG
a R R F F T S L P V Y A I I V A N F C R S -

Fig. 1 cont'd

```
        TGGACCTTCTATTTGCTCTTAATAAGTCAGCCTGCTTACTTTGAAGAGGTCTTTGGGTTT
1021    ---------+---------+---------+---------+---------+---------+ 1080
        ACCTGGAAGATAAACGAGAATTATTCAGTCGGACGAATGAAACTTCTCCAGAAACCCAAA

a           W   T   F   Y   L   L   L   I   S   Q   P   A   Y   F   E   E   V   F   G   F   -

                                BsaI PvuII          DraIII  BsaBI HphI  Acc65I
                                   |     |             |       |     |   |
        GCAATAAGTAAGGTGGGTCTCTTGTCAGCTGTCCCACACATGGTGATGACAATCGTGGTA
1081    ---------+---------+---------+---------+---------+---------+ 1140
        CGTTATTCATTCCACCCAGAGAACAGTCGACAGGGTGTGTACCACTACTGTTAGCACCAT

a           A   I   S   K   V   G   L   L   S   A   V   P   H   M   V   M   T   I   V   V   -

          KpnI
            |
        CCCATTGGAGGACAACTGGCTGATTATTTAAGAAGCCGAAAGATTTTGACCACAACTGCT
1141    ---------+---------+---------+---------+---------+---------+ 1200
        GGGTAACCTCCTGTTGACCGACTAATAAATTCTTCGGCTTTCTAAAACTGGTGTTGACGA

a           P   I   G   G   Q   L   A   D   Y   L   R   S   R   K   I   L   T   T   T   A   -

                  BspHI
                    |
        GTCAGAAAGATCATGAATTGTGGAGGCTTTGGCATGGAGGCAACCTTGCTCCTGGTGGTT
1201    ---------+---------+---------+---------+---------+---------+ 1260
        CAGTCTTTCTAGTACTTAACACCTCCGAAACCGTACCTCCGTTGGAACGAGGACCACCAA

a           V   R   K   I   M   N   C   G   G   F   G   M   E   A   T   L   L   L   V   V   -

                              BstXI
                                |
        GGGTTTTCCCATACCAAAGGAGTGGCTATCTCCTTCCTGGTGCTTGCTGTAGGATTTAGT
1261    ---------+---------+---------+---------+---------+---------+ 1320
        CCCAAAAGGGTATGGTTTCCTCACCGATAGAGGAAGGACCACGAACGACATCCTAAATCA

a           G   F   S   H   T   K   G   V   A   I   S   F   L   V   L   A   V   G   F   S   -

        GGCTTTGCAATTTCAGGTTTCAATGTCAACCACCTGGACATTGCTCCACGATATGCCAGC
1321    ---------+---------+---------+---------+---------+---------+ 1380
        CCGAAACGTTAAAGTCCAAAGTTACAGTTGGTGGACCTGTAACGAGGTGCTATACGGTCG

a           G   F   A   I   S   G   F   N   V   N   H   L   D   I   A   P   R   Y   A   S   -

          XcmI
            |
        ATCCTCATGGGGATCTCAAATGGCGTGGGAACCCTCTCTGGAATGGTTTGTCCCCTCATT
1381    ---------+---------+---------+---------+---------+---------+ 1440
        TAGGAGTACCCCTAGAGTTTACCGCACCCTTGGGAGAGACCTTACCAAACAGGGGAGTAA

a           I   L   M   G   I   S   N   G   V   G   T   L   S   G   M   V   C   P   L   I   -
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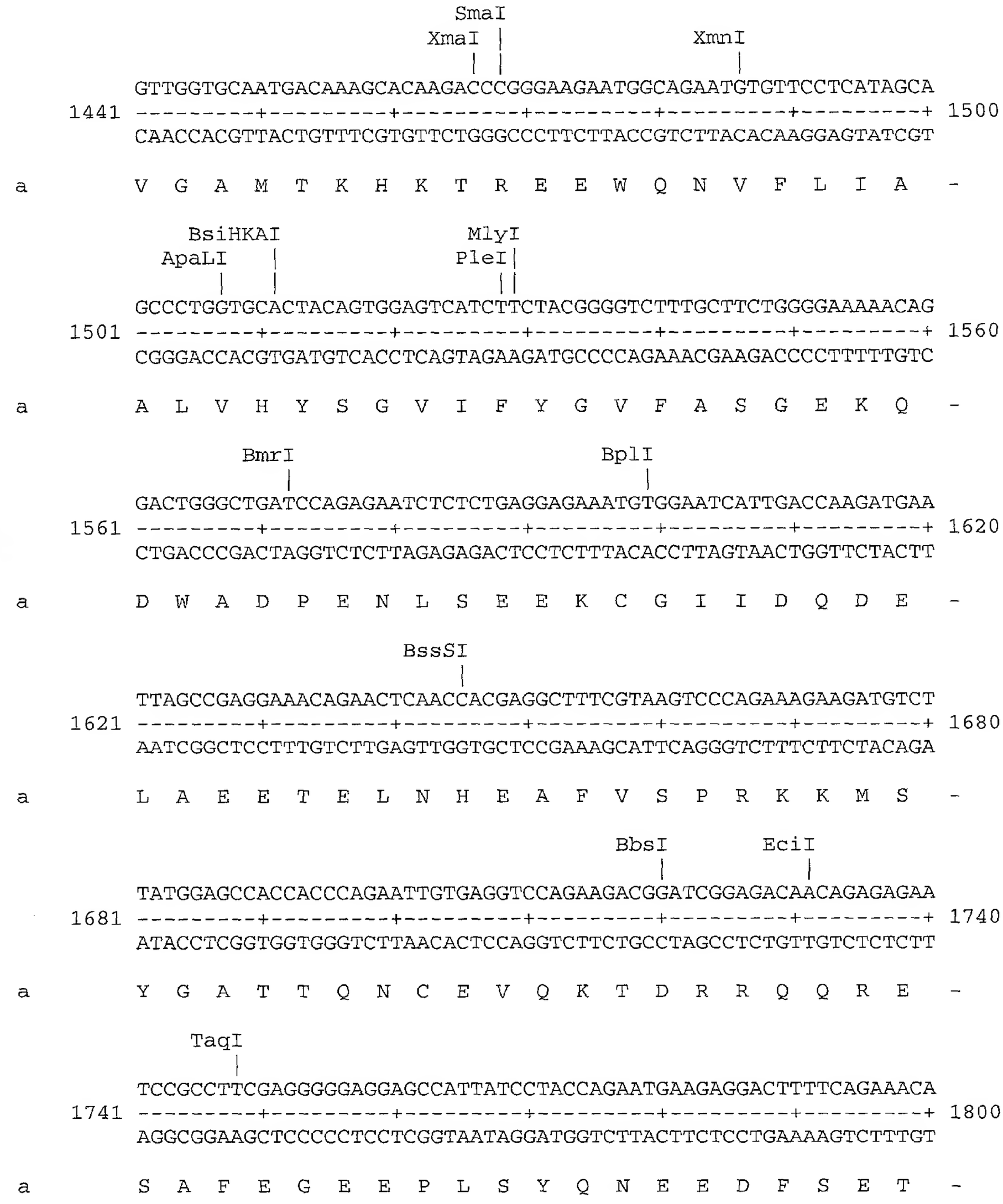
Fig. 1 cont'd


SmaI
XmaI
XmnI
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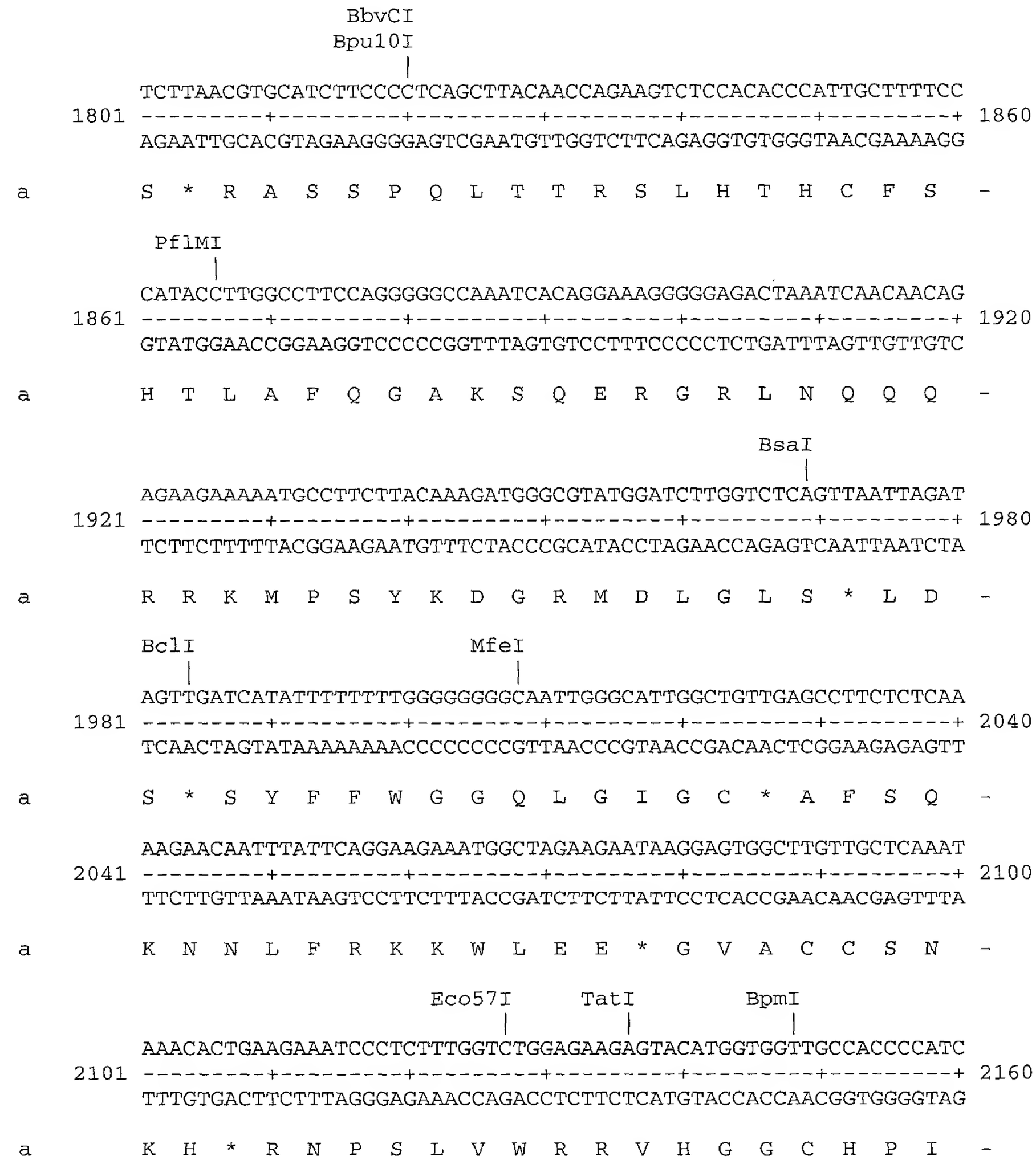
1441 ----------+----------+----------+----------+----------+----------+---------- 1500
CAACCACGTTACTGTTTCGTGTTCTGGGCCCTTCTTACCGTCTTACACAAGGAGTATCGT
a V G A M T K H K T R E E W Q N V F L I A -
BsiHKAI
ApaLI
MlyI
PleI
GCCCTGGTGCACTACAGTGGAGTCATCTTCTACGGGGTCTTTGCTTCTGGGGAAAAACAG
1501 ----------+----------+----------+----------+----------+----------+---------- 1560
CGGGACCACGTGATGTCACCTCAGTAGAAGATGCCCCAGAAACGAAGACCCCTTTTTGTC
a A L V H Y S G V I F Y G V F A S G E K Q -
BmrI
BplI
GACTGGGCTGATCCAGAGAATCTCTCTGAGGAGAAATGTGGAATCATTGACCAAGATGAA
1561 ----------+----------+----------+----------+----------+----------+---------- 1620
CTGACCCGACTAGGTCTCTTAGAGAGACTCCTCTTTACACCTTAGTAACTGGTTCTACTT
a D W A D P E N L S E E K C G I I D Q D E -
BssSI
TTAGCCGAGGAAACAGAACTCAACCACGAGGCTTTCGTAAGTCCCAGAAAGAAGATGTCT
1621 ----------+----------+----------+----------+----------+----------+---------- 1680
AATCGGCTCCTTTGTCTTGAGTTGGTGCTCCGAAAGCATTCAGGGTCTTTCTTCTACAGA
a L A E E T E L N H E A F V S P R K K M S -
BbsI
EciI
TATGGAGCCACCACCCAGAATTGTGAGGTCCAGAAGACGGATCGGAGACAACAGAGAGAA
1681 ----------+----------+----------+----------+----------+----------+---------- 1740
ATACCTCGGTGGTGGGTCTTAACACTCCAGGTCTTCTGCCTAGCCTCTGTTGTCTCTCTT
a Y G A T T Q N C E V Q K T D R R Q Q R E -
TaqI
TCCGCCTTCGAGGGGGAGGAGCCATTATCCTACCAGAATGAAGAGGACTTTTCAGAAACA
1741 ----------+----------+----------+----------+----------+----------+---------- 1800
AGGCGGAAGCTCCCCCTCCTCGGTAATAGGATGGTCTTACTTCTCCTGAAAAGTCTTTGT
a S A F E G E E P L S Y Q N E E D F S E T -

Fig. 1 cont'd


BbvCI
Bpu10I
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1801 ----------+----------+----------+----------+----------+----------+---------- 1860
AGAATTGCACGTAGAAGGGGAGTCGAATGTTGGTCTTCAGAGGTGTGGGTAACGAAAAGG
a S * R A S S P Q L T T R S L H T H C F S -
PflMI
CATACCTTGGCCTTCCAGGGGGCCAAATCACAGGAAAGGGGGAGACTAAATCAACAACAG
1861 ----------+----------+----------+----------+----------+----------+---------- 1920
GTATGGAACCGGAAGGTCCCCCGGTTTAGTGTCCTTTCCCCCTCTGATTTAGTTGTTGTC
a H T L A F Q G A K S Q E R G R L N Q Q Q -
BsaI
AGAAGAAAAATGCCTTCTTACAAAGATGGGCGTATGGATCTTGGTCTCAGTTAATTAGAT
1921 ----------+----------+----------+----------+----------+----------+---------- 1980
TCTTCTTTTTACGGAAGAATGTTTCTACCCGCATACCTAGAACCAGAGTCAATTAATCTA
a R R K M P S Y K D G R M D L G L S * L D -
BclI
MfeI
AGTTGATCATATTTTTTTGGGGGGGGCAATTGGGCATTGGCTGTTGAGCCTTCTCTCAA
1981 ----------+----------+----------+----------+----------+----------+---------- 2040
TCAACTAGTATAAAAAAAACCCCCCCCGTTAACCCGTAACCGACAACTCGGAAGAGAGTT
a S * S Y F F W G G Q L G I G C * A F S Q -
AAGAACAATTTATTCAGGAAGAAATGGCTAGAAGAATAAGGAGTGGCTTGTTGCTCAAAT
2041 ----------+----------+----------+----------+----------+----------+---------- 2100
TTCTTGTTAAATAAGTCCTTCTTTACCGATCTTCTTATTCCTCACCGAACAACGAGTTTA
a K N N L F R K K W L E E * G V A C C S N -
Eco57I
TatI
BpmI
AAACACTGAAGAAATCCCTCTTTGGTCTGGAGAAGAGTACATGGTGGTTGCCACCCCATC
2101 ----------+----------+----------+----------+----------+----------+---------- 2160
TTTGTGACTTCTTTAGGGAGAAACCAGACCTCTTCTCATGTACCACCAACGGTGGGGTAG
a K H * R N P S L V W R R V H G G C H P I -

Fig. 1 cont'd

```
                                                              Eco0109I
          EcoRV                          EcoNI                PspOMI
            |                              |                       |
     TCCAAGGATATCCATGTAGAGGACAATCTCTGCAACCTAATGAAGGGAATCACTCATGGG
2161 ---------+---------+---------+---------+---------+---------+ 2220
     AGGTTCCTATAGGTACATCTCCTGTTAGAGACGTTGGATTACTTCCCTTAGTGAGTACCC

a    S  K  D  I  H  V  E  D  N  L  C  N  L  M  K  G  I  T  H  G   -

     ApaI
 Eco0109I |
     |    |
     GGCCCTTGGTTGTGCCAGGTGCTTTATGAACATTCTTATTTAACTCCCACACCCTAATAT
2221 ---------+---------+---------+---------+---------+---------+ 2280
     CCGGGAACCAACACGGTCCACGAAATACTTGTAAGAATAAATTGAGGGTGTGGGATTATA

a    G  P  W  L  C  Q  V  L  Y  E  H  S  Y  L  T  P  T  P  *  Y   -

     AGTTATTGTACCCATTTTACAACTAAGAACATTAAATGACTAGGTTGGCCCACCCAAGGT
2281 ---------+---------+---------+---------+---------+---------+ 2340
     TCAATAACATGGGTAAAATGTTGATTCTTGTAATTTACTGATCCAACCGGGTGGGTTCCA

a    S  Y  C  T  H  F  T  T  K  N  I  K  *  L  G  W  P  T  Q  G   -

     TGTCCTCTCAGAGCCAAAGCTGAGACTGGCAGATGACCAGGAGTTTTAGGAAGGAAGGAA
2341 ---------+---------+---------+---------+---------+---------+ 2400
     ACAGGAGAGTCTCGGTTTCGACTCTGACCGTCTACTGGTCCTCAAAATCCTTCCTTCCTT

a    C  P  L  R  A  K  A  E  T  G  R  *  P  G  V  L  G  R  K  E   -

     GGAAGGAAGGAAGGAAGGAAGGAAGGAAGGAAGGAAGGAAGGAAGGGTTCAGTTGAGTGT
2401 ---------+---------+---------+---------+---------+---------+ 2460
     CCTTCCTTCCTTCCTTCCTTCCTTCCTTCCTTCCTTCCTTCCTTCCCAAGTCAACTCACA

a    G  R  K  E  G  R  K  E  G  R  K  E  G  R  K  G  S  V  E  C   -

     AGGGTCATTTTCAATGACAAAAACAAAAACTGGAATCAGTTGGTTTGTGGGTAATTCCAT
2461 ---------+---------+---------+---------+---------+---------+ 2520
     TCCCAGTAAAAGTTACTGTTTTTGTTTTTGACCTTAGTCAACCAAACACCCATTAAGGTA

a    R  V  I  F  N  D  K  N  K  N  W  N  Q  L  V  C  G  *  F  H   -

                         SphI
                           |
     GTTTGGTCAAGGGTGTGTGCATGCAAACGTGTATGTGCGTGTGTGTGTGTTTGTGTGTTT
2521 ---------+---------+---------+---------+---------+---------+ 2580
     CAAACCAGTTCCCACACACGTACGTTTGCACATACACGCACACACACACAAACACACAAA

a    V  W  S  R  V  C  A  C  K  R  V  C  A  C  V  C  V  C  V  F   -
```

Fig. 1 cont'd

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      GNGTGTNAGNNNGNATNANAANAAAAN
2581  ---------+---------+------- 2607
      CNCACANTCNNNCNTANTNTTNTTTTN
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Fig. 1 cont'd

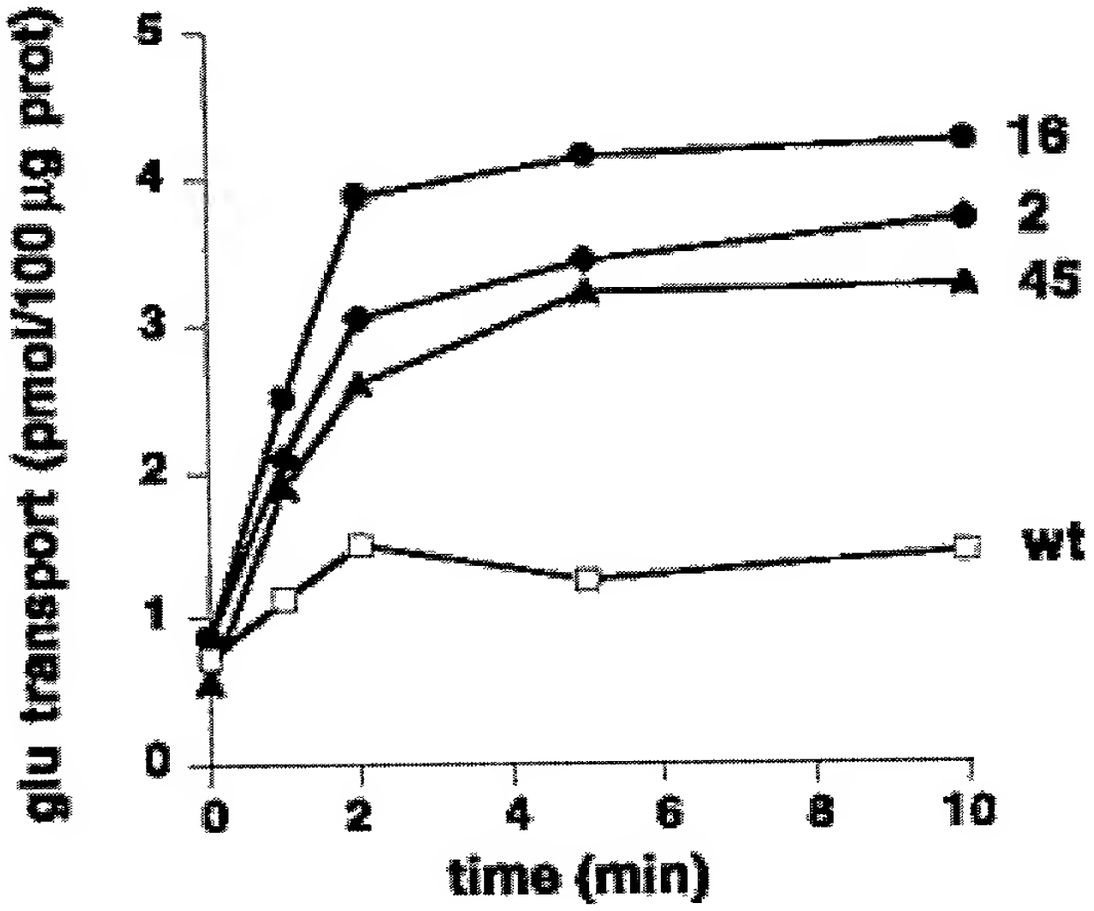

glu transport (pmol/100 µg prot)
time (min)
0
1
2
3
4
5
0
2
4
6
8
10
16
2
45
wt

Fig. 2A

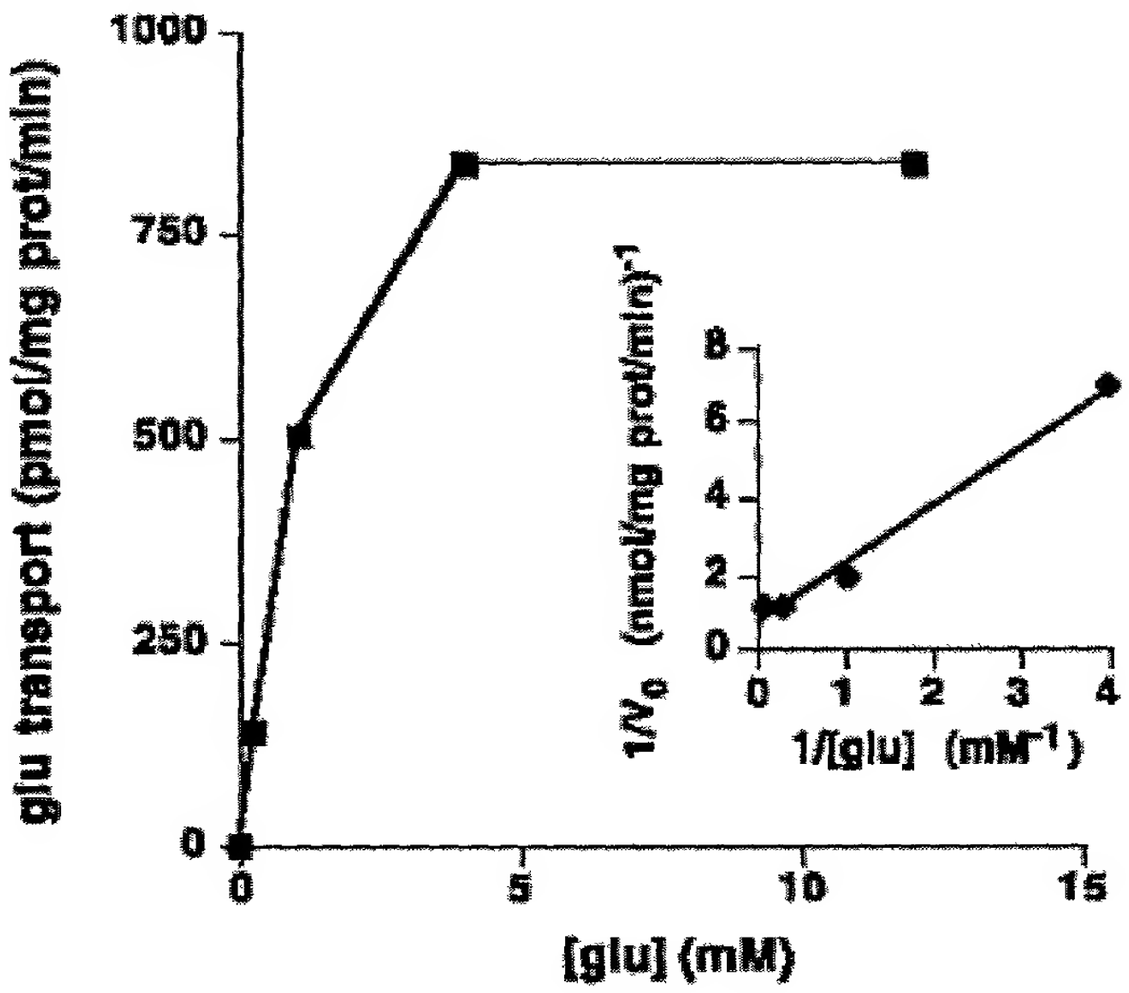

glu transport (pmol/mg prot/min)
1000
750
500
250
0
0
5
10
15
[glu] (mM)
1/V0 (nmol/mg prot/min)-1
8
6
4
2
0
0
1
2
3
4
1/[glu] (mM-1)

Fig. 2B

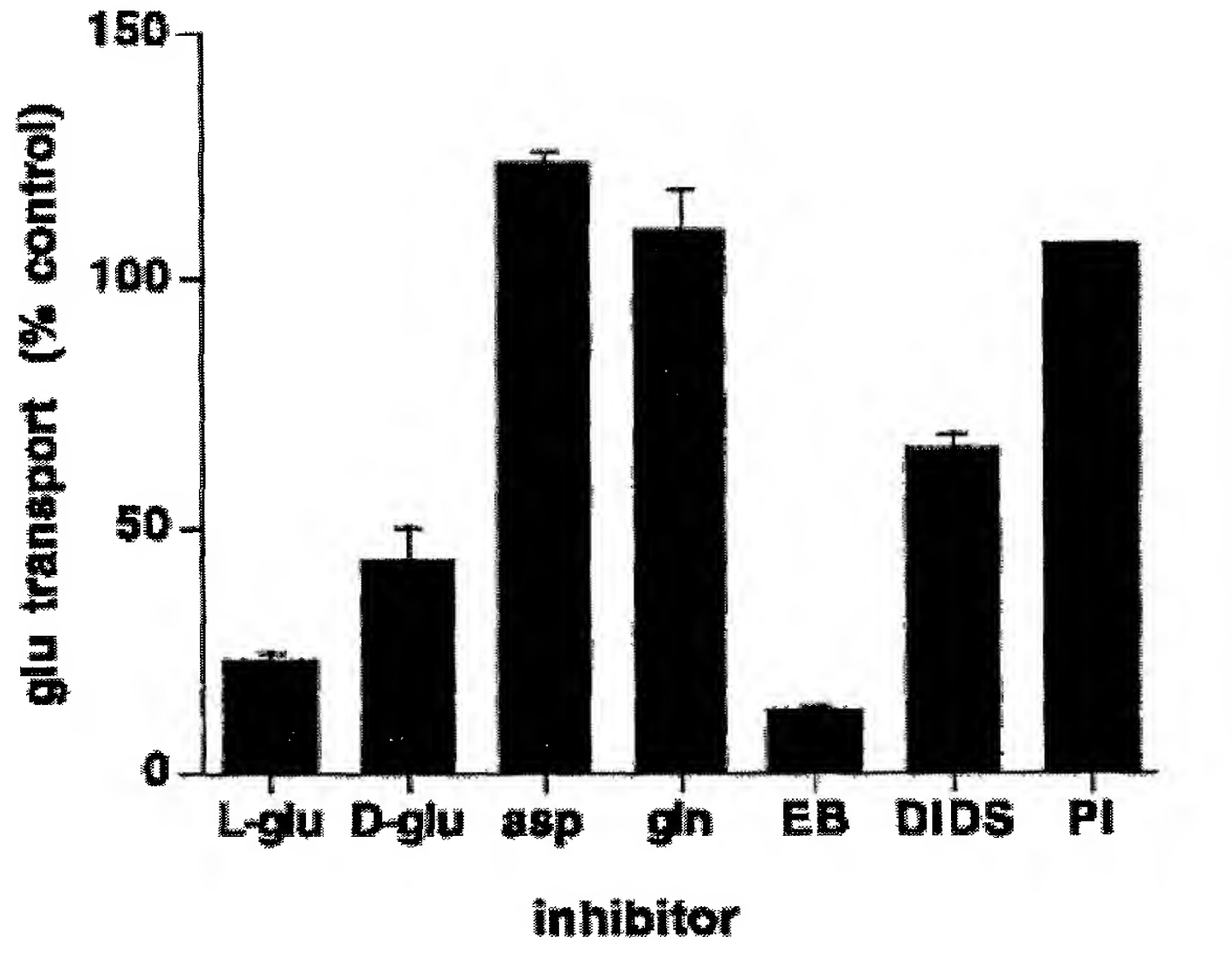

150
100
50
0
glu transport (% control)
L-glu
D-glu
asp
gln
EB
DIDS
PI
inhibitor

Fig. 3

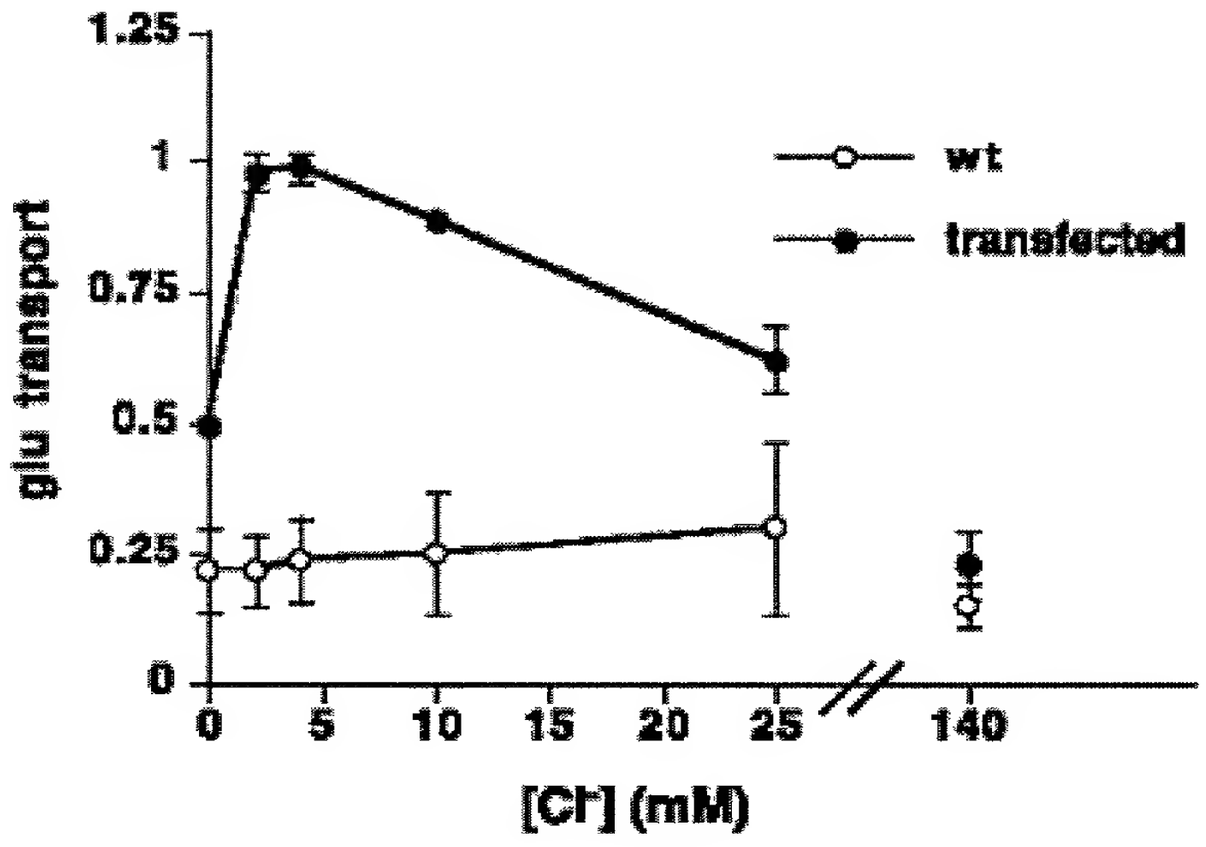

1.25
1
0.75
0.5
0.25
0
glu transport
wt
transfected
0
5
10
15
20
25
140
[Cl-] (mM)

Fig. 4A

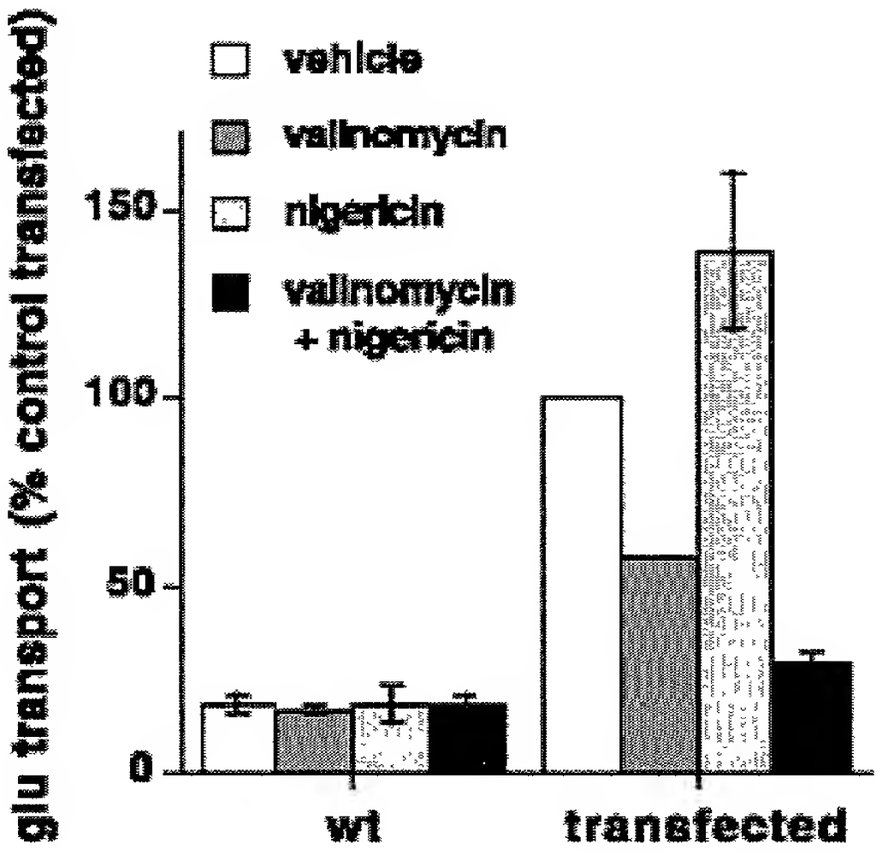

glu transport (% control transfected)
150
100
50
0
vehicle
valinomycin
nigericin
valinomycin + nigericin
wt
transfected

Fig. 4B

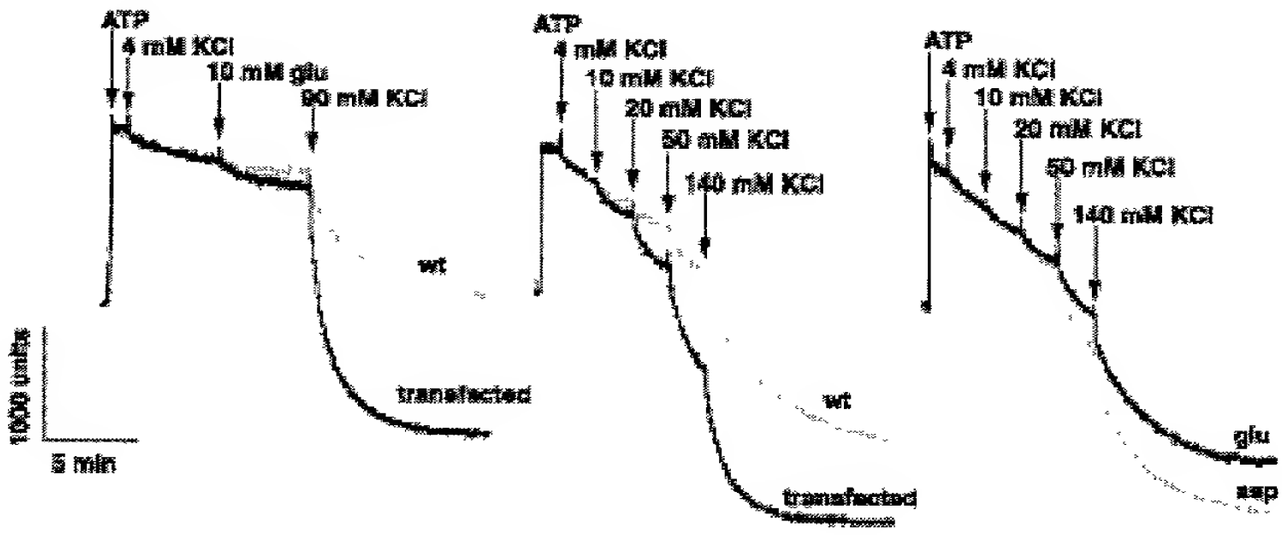


Fig. 5A *Fig. 5B* *Fig. 5C*

Fig. 5A, 5B, and 5C

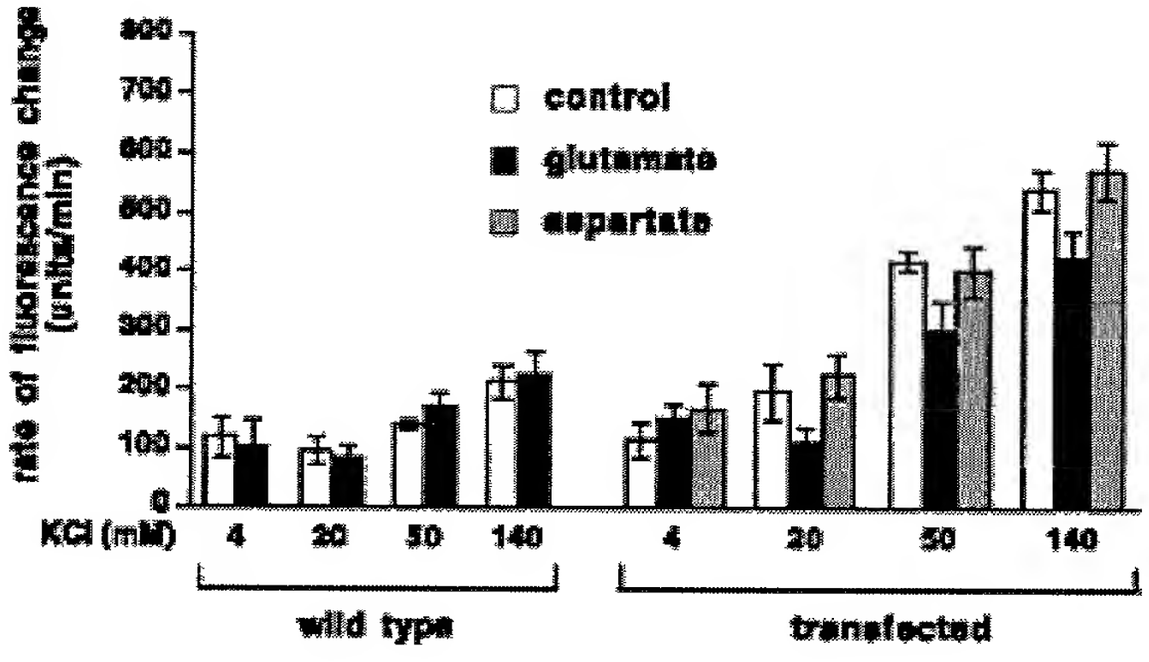

rate of fluorescence change (units/min)
800
700
600
500
400
300
200
100
0
control
glutamate
aspartate
KCl (mM)
4
20
50
140
4
20
50
140
wild type
transfected

Fig. 5D

```
rVGLUT2 MESVKQRILAPGKEGIKNFAGKSLGQIYRVLEKKQDNRETIELTE.DG..KPLEVPEKKA.PLCDCTCF.....GLPR.RYIIAIMSGLG  80
rVGLUT1       MEFRQEEFRKLAGRALGRLHRLLEKRQEGAETLELSA.DG..RPVTTHTRDP.PVVDCTCF.....GLPR.RYIIAIMSGLG  72
   EAT4             MVGEPLAKMTAAAASATGAAPPQQMQE.EGNENPMQMHSNKVLQVMEQTWI.....GKCRKRWLLAILANMG  66
hsialin                                        MRSPVRDLARNDGEESTDRTPLLPGAPRAEAAPV......CCSARYNLAILAFFG  49
 rNaPi1                                                                MENRCLPKKVPGFCSFRYGLAILLHFC  27

rVGLUT2 FCISFGIRCNLGVAIVDMVNNSTI..........HRGGKVIKEKAK....FNWDPETVGMIHGSFFWGYIITQIPGGYIASRLAANRVF 155
rVGLUT1 FCISFGIRCNLGVAIVSMVNNSTT..........HRGGHVVVQKAQ....FNWDPETVGLIHGSFFWGYIVTQIPGGFICQKFAANRVF 147
   EAT4 FMISFGIRCNFGAAKTHMYKNYTD..........PYGK...VHMHE....FNWTIDELSVMESSYFYGYLVTQIPAGFLAAKFPPNKLF 138
hsialin FFIVYALRVNLSVALVDMVDSNTTLEDNRTSKACPEHSAPIKVHHNQTGKKYQWDAETQGWILGSFFYGYIITQIPGGYVASKIGGKMLL 139
 rNaPi1 NIVIMAQRVCLNLTMVAMVNKTEPPHLSNKSVAEMLDNVKNPVH........SWSLDIQGLVLSSVFLGMVVIQVPVGYLSGAYPMEKII 109

rVGLUT2 GAAILLTSTLNMLIPSAARVHYG.CVIFVRILQGLVEGVTYPACHGIWSKWAPPLERSRLATTSFCGSYAGAVIAMPLAGILVQYTGWSS 244
rVGLUT1 GFAIVATSTLNMLIPSAARVHYG.CVIFVRILQGLVEGVTYPACHGIWSKWAPPLERSRLATTAFCGSYAGAVVAMPLAGVLVQYSGWSS 236
   EAT4 GFGIGVGAFLNILLPYGFKVKSDYLVAFIQITQGLVQGVCYPAMHGVWRYWAPPMERSKLATTAFTGSYAGAVLGLPLSAFLVSYVSWAA 228
hsialin GFGILGTAVLTLFTPIAADLGVGPLIV.LRALEGLGEGVTFPAMHAMWSSWAPPLERSKLLSISYAGAQLGTVISLPLSGIICYYMNWTY 228
 rNaPi1 GSSLFLSSVLSLLIPPAAQVG.AALVIVCRVLQGIAQGAVSTGQHGIWVKWAPPLERGRLTSMTLSGFVMGPFIALLVSGFICDLLGWPM 198

rVGLUT2 VFYVYGSFGMVWYMFWLLVSYESPAKHPTITDEERRYIEESIGESANLLGAMEKFKTPWRKFFTSMPVYAIIVANFCRSWTFYLLLISQP 334
rVGLUT1 VFYVYGSFGIFWYLFWLLVSYESPALHPSISEEERKYIEDAIGESAKLMNPVTKFNTPWRRFFTSMPVYAIIVANFCRSWTFYLLLISQP 326
   EAT4 PFYLYGVCGVIWAILWFCVTFEKPAFHPTISQEEKIFIEDAIGHVSNTHPTIRSI..PWKAIVTSKPVWAIIVANFARSWTFYLLLQNQL 316
hsialin VFYFFGTIGIFWFLLWIWLVSDTPQKHKRISHYEKEYILSSLRNQLSSQKSV.....PWVPILKSLPLWAIVVAHFSYNWTFYTLLTLLP 313
 rNaPi1 VFYIFGIVGCVLSLFWFILLFDDPNNHPYMSSSEKDYITSSLMQQVHS....GRQSLPIKAMLKSLPLWAIILNSFAFIWSNNLLVTYTP 284

rVGLUT2 AYFEEVFGFEISKVGMLSAVPHLVMTIIVPIGGQIADFLRSKQILSTTTVRKIMNCGGFGMEATLLLVVGYSHTR.GVAISFLVLAVGFS 423
rVGLUT1 AYFEEVFGFEISKVGLVSALPHLVMTIIVPIGGQIADFLRSRHIMSTTNVRKLMNCGGFGMEATLLLVVGYSHSK.GVAISFLVLAVGFS 415
   EAT4 TYMKEALGMKIADSGLLAAIPHLVMGCVVLMGGQLADYLRSNKILSTTAVRKIFNCGGFGGEAAFMLIVAYTTSD.TTAIMALIAAVGMS 405
hsialin TYMKEILRFNVQENGFLSSLPYLGSWLCMILSGQAADNLRAKWNFSTLCVRRIFSLIGMIGPAVFLVAAGFIGCDYSLAVAFLTISTTLG 403
 rNaPi1 TFISTTLHVNVRENGLLSSLPYLLAYICGIVAGQMSDFLLSRKIFSVVAVRKLFTTLGIFCPVIFVVCLLYLSYNFYSTVIFLTLANSTL 374

rVGLUT2 GFAISGFNVNHLDIAPRYASILMGISNGVGTLSGMVCPIIVGAMTKNKSREEWQYVFLIAALVHYGGVIFYALFASGEKQPWADPEETSE 513
rVGLUT1 GFAISGFNVNHLDIAPRYASILMGISNGVGTLSGMVCPIIVGAMTKHKTREEWQYVFLIASLVHYGGVIFYGVFASGEKQPWAEPEEMSE 505
   EAT4 GFAISGFNVNHLDIAPRYAAILMGFSNGIGTLAGLTCPFVTEAFTAH.SKHGWTSVFLLASLIHFTGVTFYAVYASGELQEWAEPKEEEE 494
hsialin GFCSSGFSINHLDIAPSYAGILLGITNTFATIPGMVGPVIAKSLTPDNTVGEWQTVFYIAAAINVFGAIFFTLFAKGEVQNWALNDHHGH 493
 rNaPi1   FSFCGQLINALDIAPRYYGFLKAVTALIGIFGGLISSTLAGLILNQDPEYAWHKNFFLMAGINVTCLAFYLLFAKGDIQDWAKETKTTR 464

rVGLUT2 .EKCGFIHEDEL.....DEETGDITQNYINYGTTKSYGATSQENGGWPNGWEKKEEFVQESAQDAYSYKDRDDYS582
rVGLUT1 .EKCGFVGHDQLAGSDESEMEDEVEPPGAPPAPPPSYGAT.HSTVQPPRPPPPPVRDY                    560
   EAT4 WSNKELVNKTGINGTGYGAAETTFTQ..LPAGVDSSYQAQAAPAPGTNPFASAWDEHGSSGVVENPHYQQW          563
hsialin RH                                                                            495
 rNaPi1 L                                                                             465
```

Fig. 6A

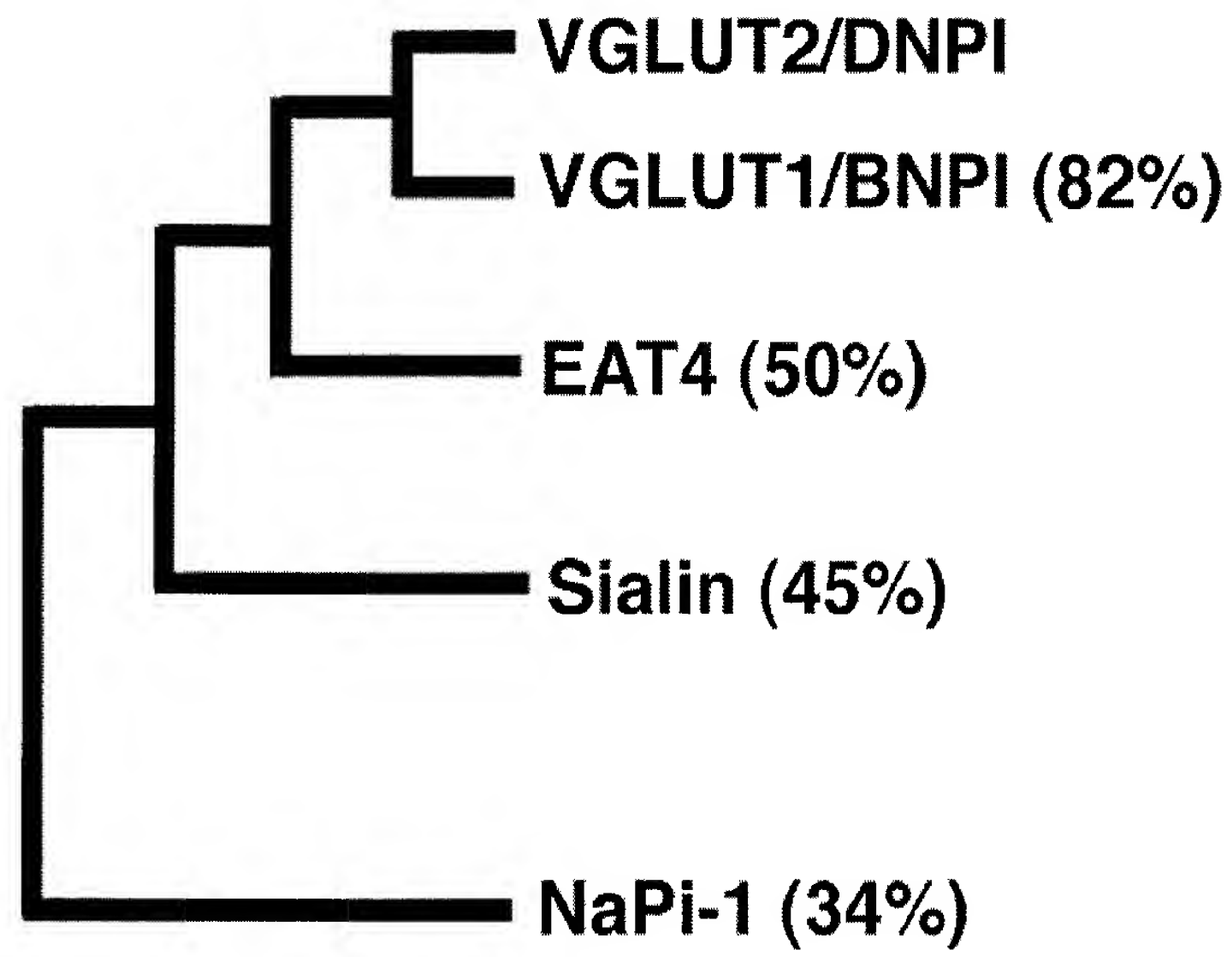


Fig. 6B

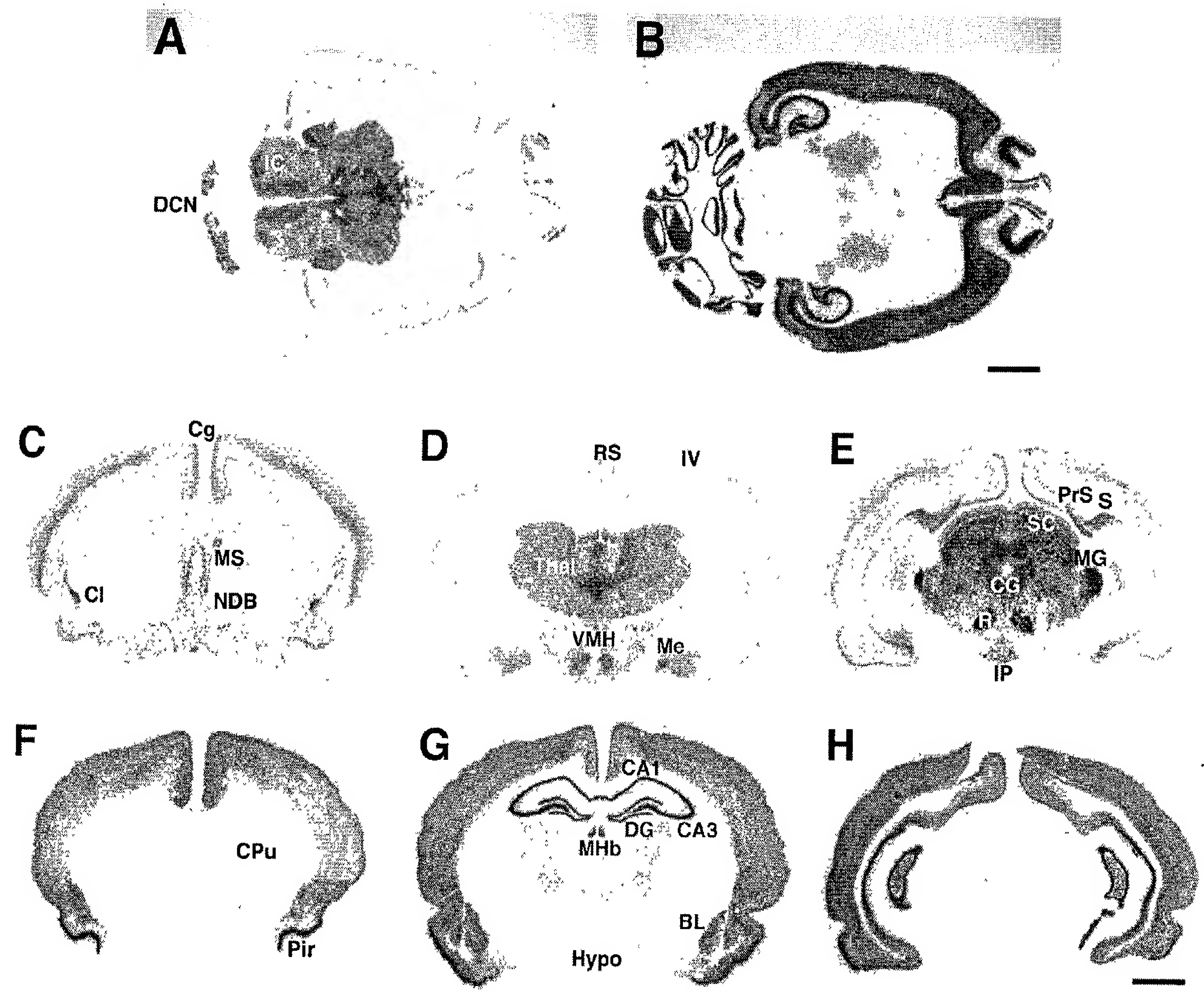

A
IC
DCN
B
C
Cg
MS
Cl
NDB
D
RS
IV
Thal
VMH
Me
E
PrS
S
SC
MG
CG
R
IP
F
CPu
Pir
G
CA1
DG
CA3
MHb
BL
Hypo
H

Fig. 7

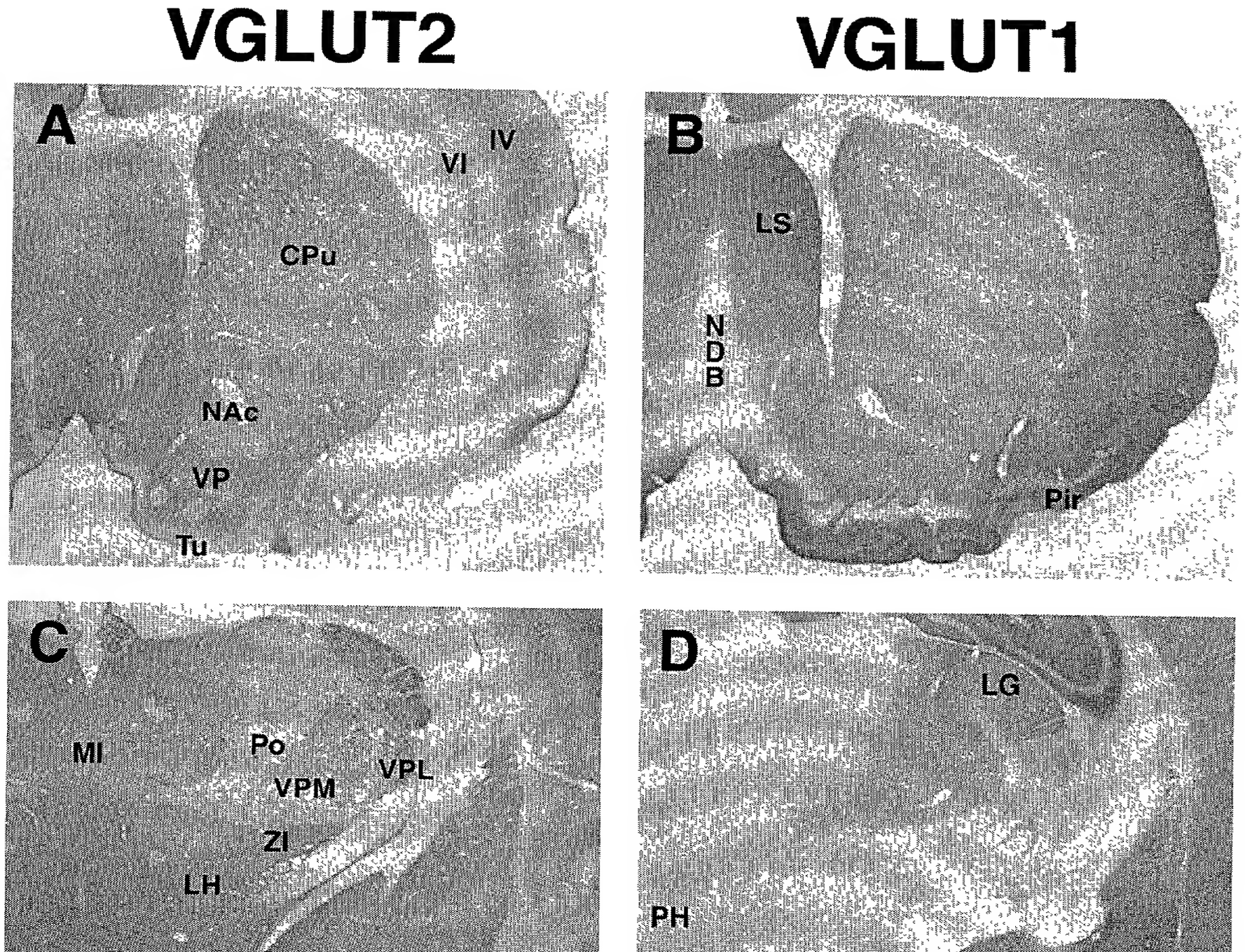

VGLUT2
VGLUT1
A
IV
VI
CPu
NAc
VP
Tu
B
LS
NDB
Pir
C
MI
Po
VPM
VPL
ZI
LH
VMH
A
D
LG
PH
E
SC
CG
F
PrS
S
MG
HC
SNc
SNr
MM

Fig. 8

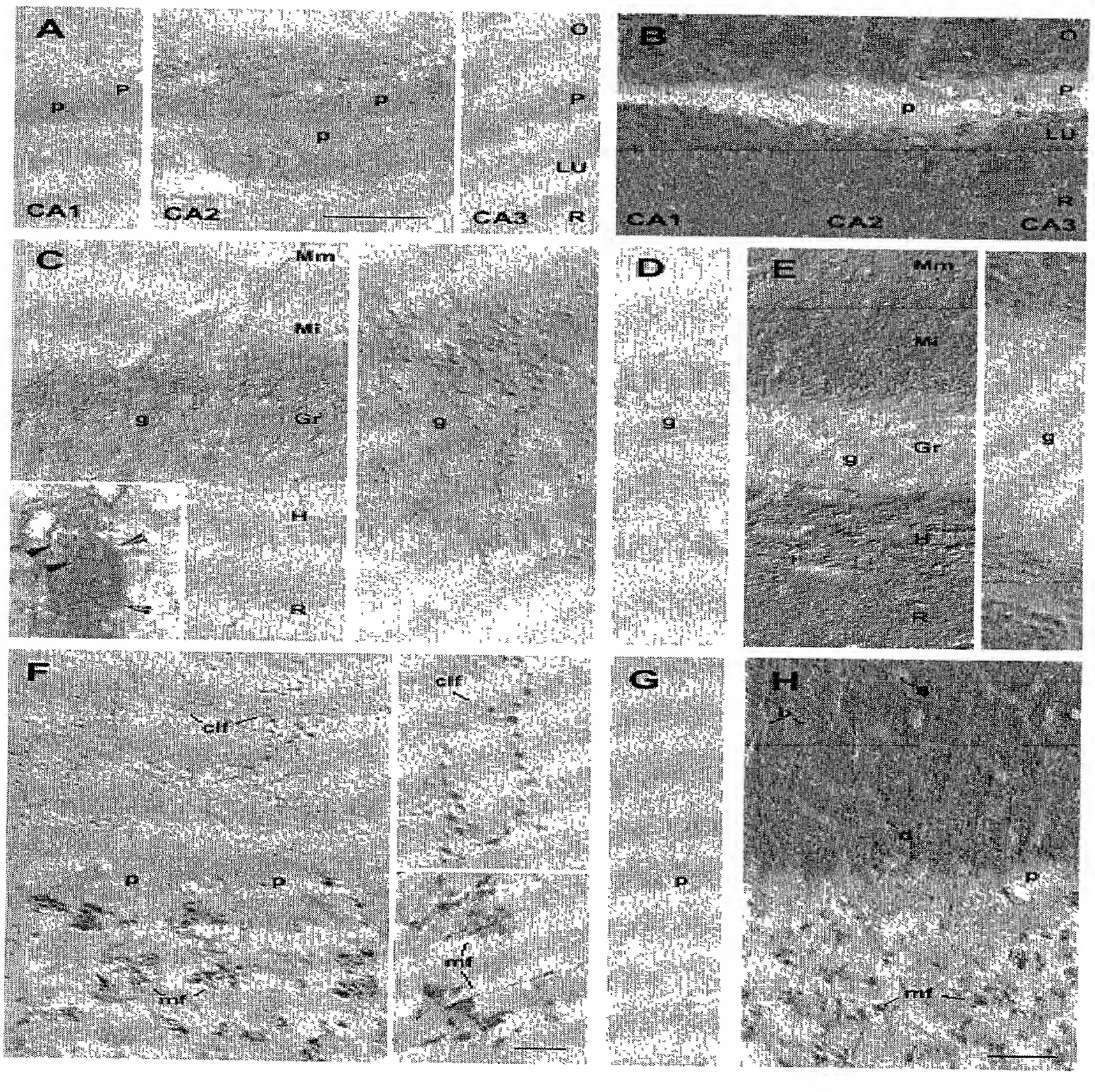

A
P
p
p
p
CA1
CA2
O
P
LU
CA3
R
B
O
P
p
LU
R
CA1
CA2
CA3
C
Mm
Mi
g
Gr
H
R
g
D
g
E
Mm
Mi
g
Gr
H
R
g
F
clf
p
p
mf
clf
mf
G
p
H
g
b
a
p
mf

Fig. 9

Fig. 10A

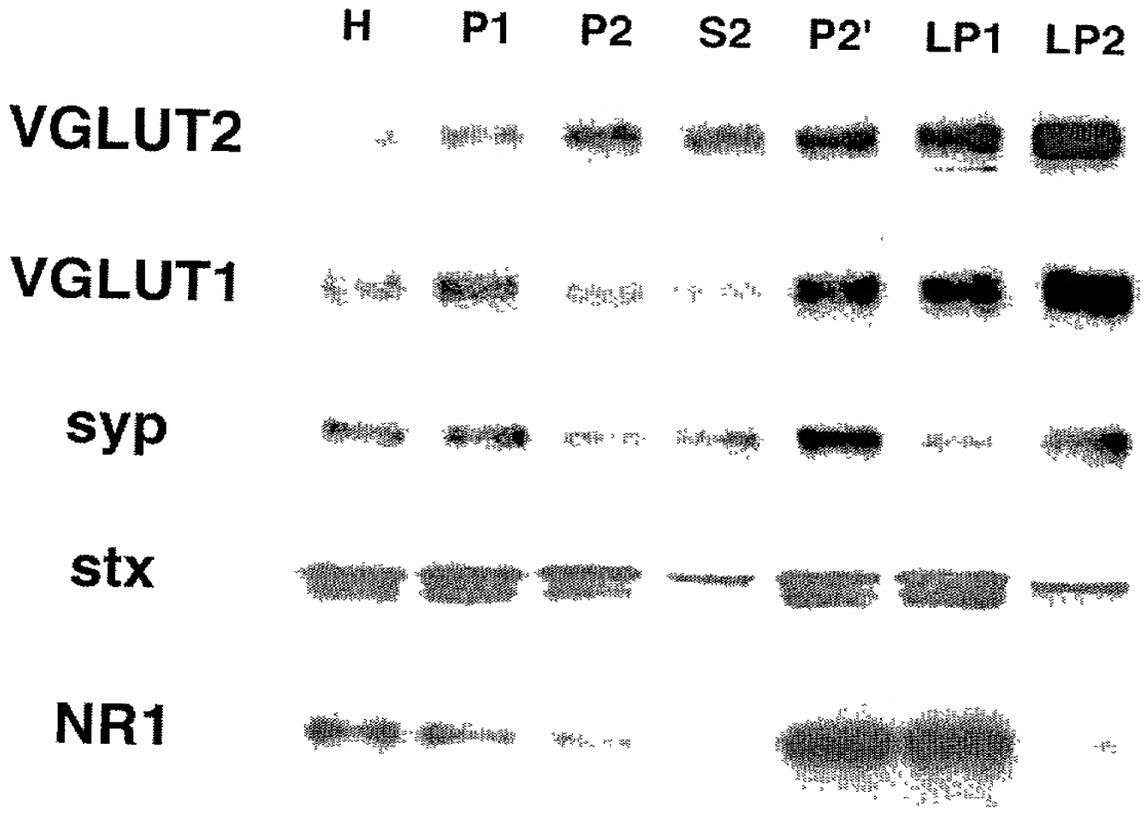


Fig. 10B

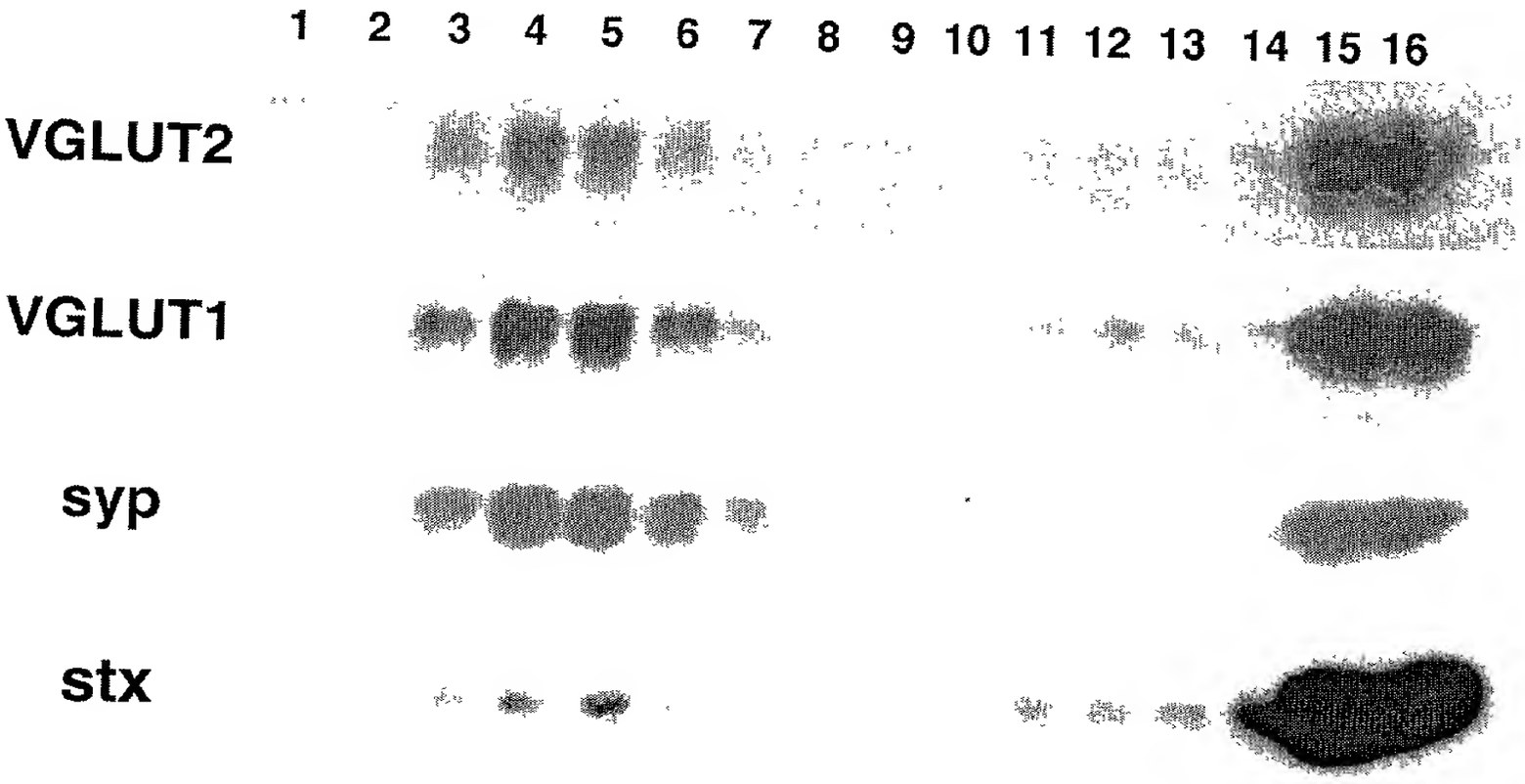
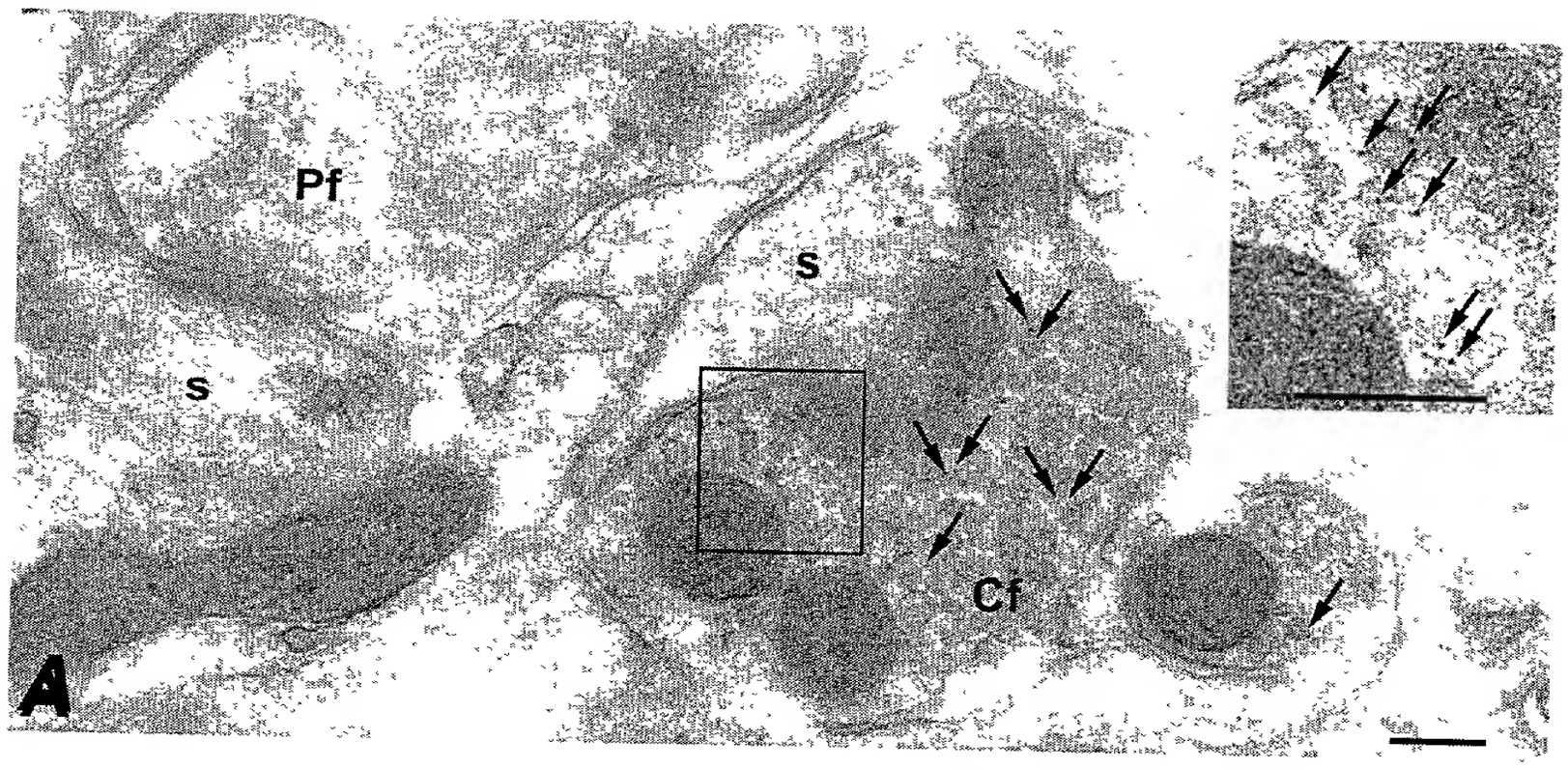


Fig. 11A



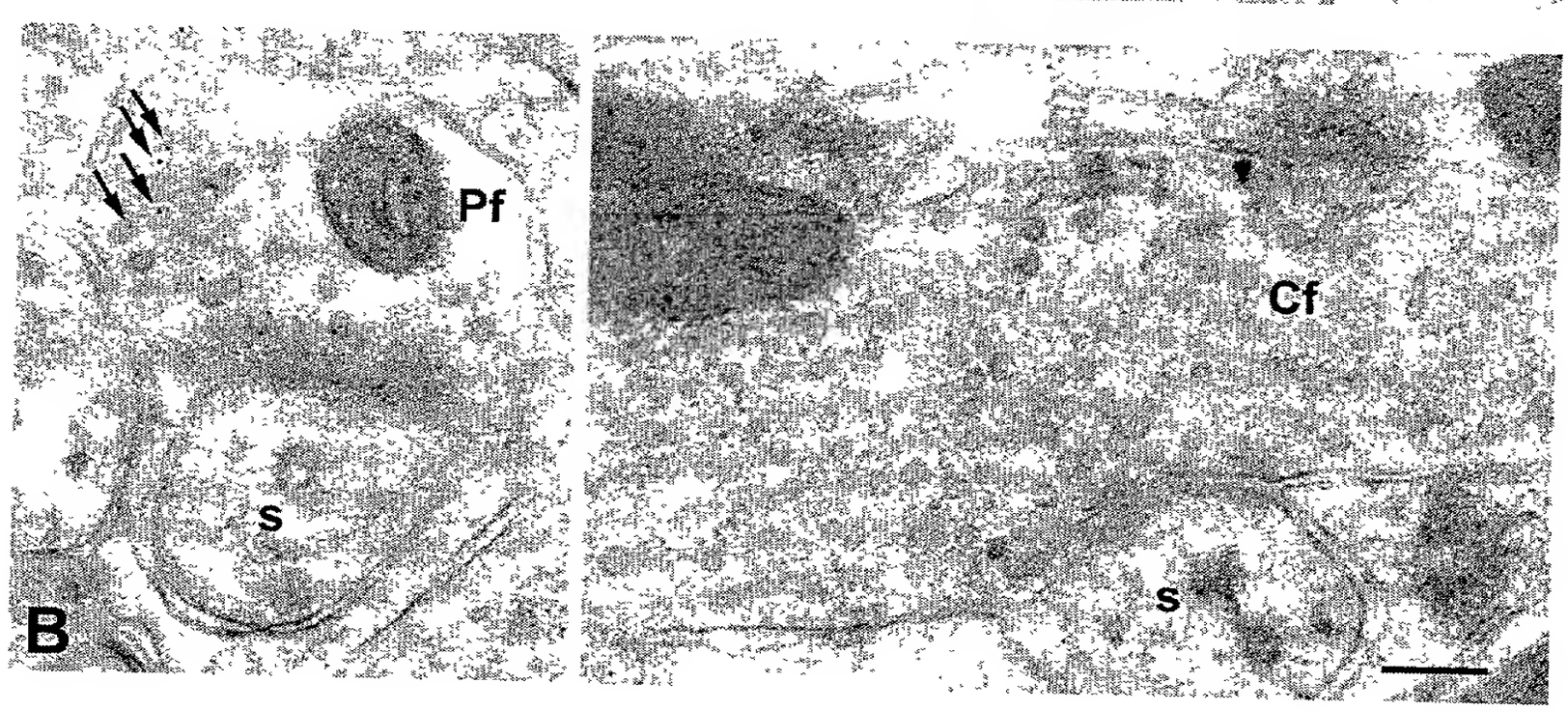


Fig. 11B

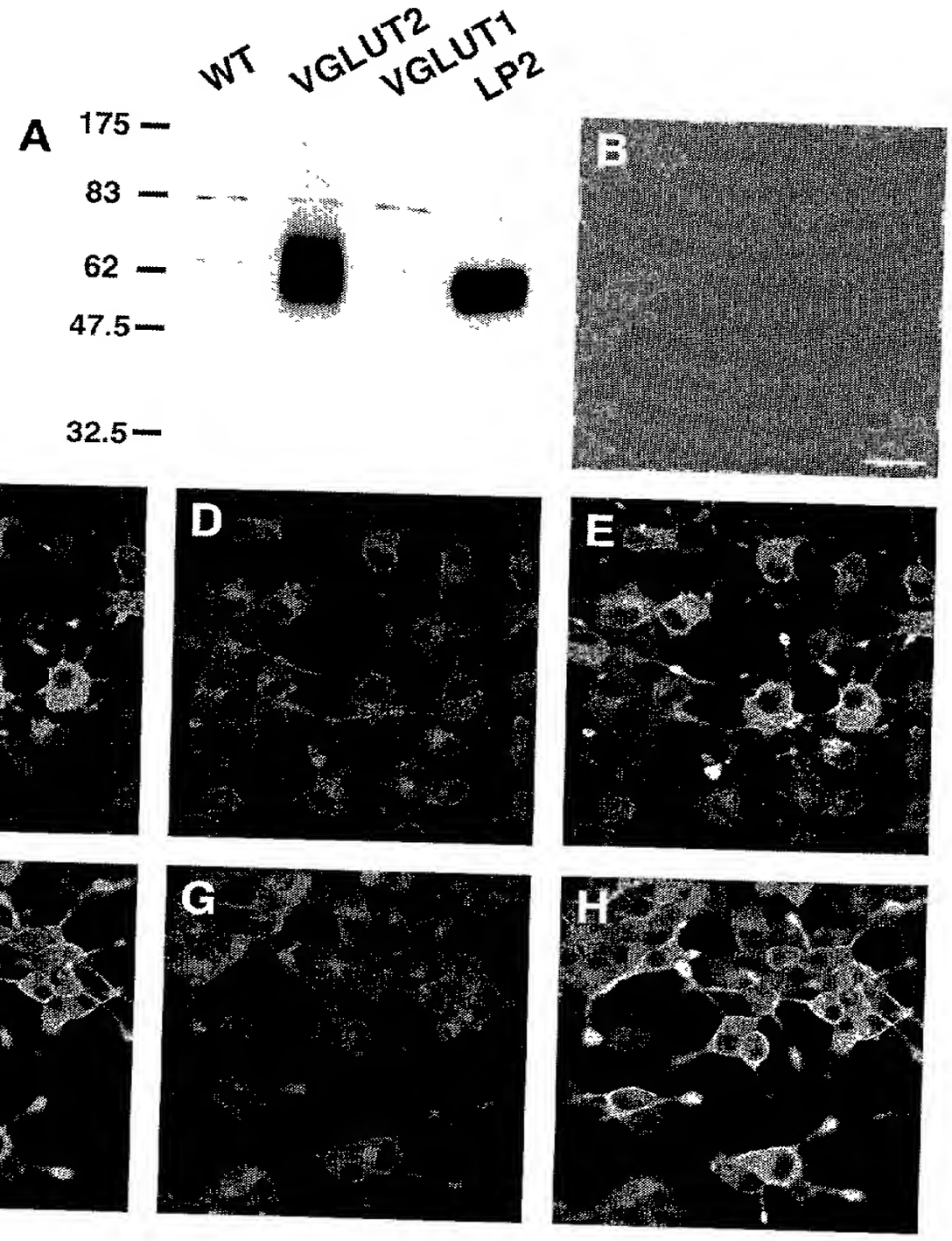

WT
VGLUT2
VGLUT1
LP2
A
175
83
62
47.5
32.5
B
C
D
E
F
G
H
VGLUT2
VGLUT1

Fig. 12

Fig. 13A

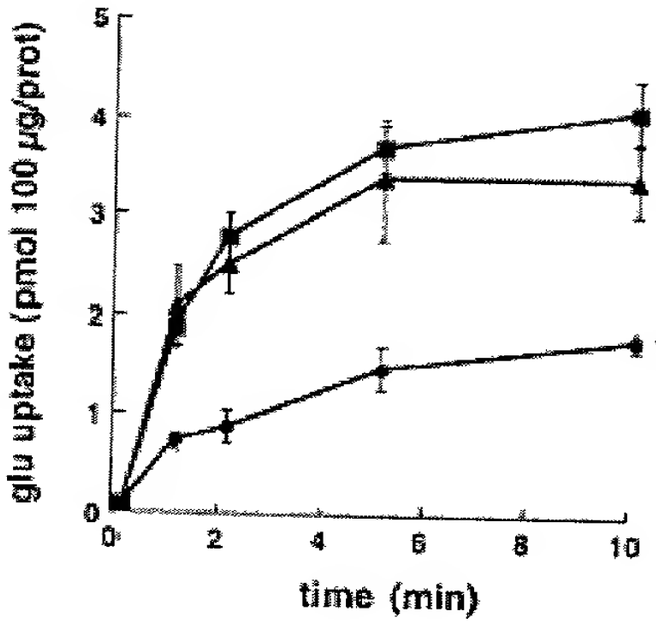
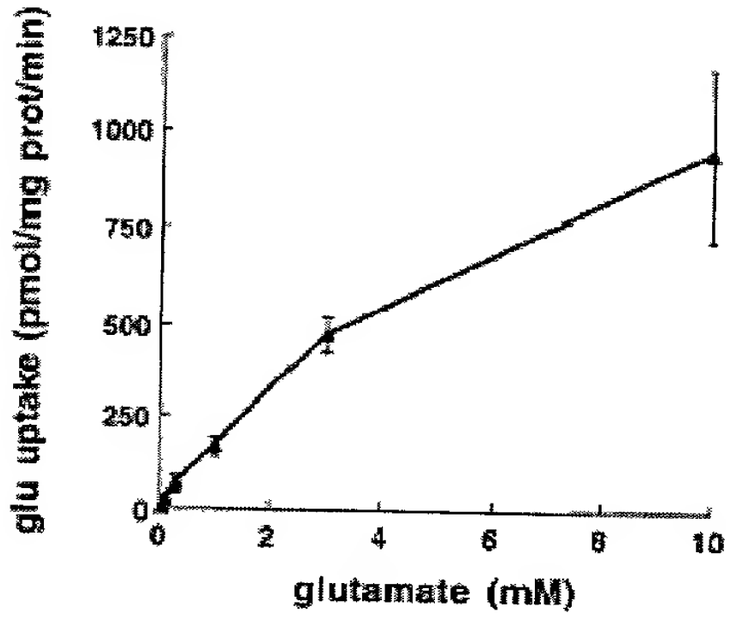


Fig. 13B



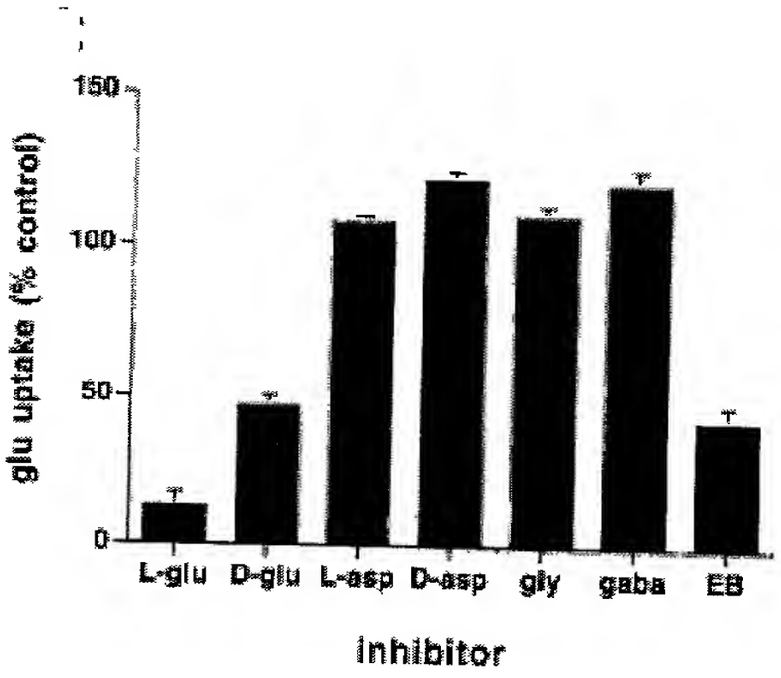


Fig. 13C

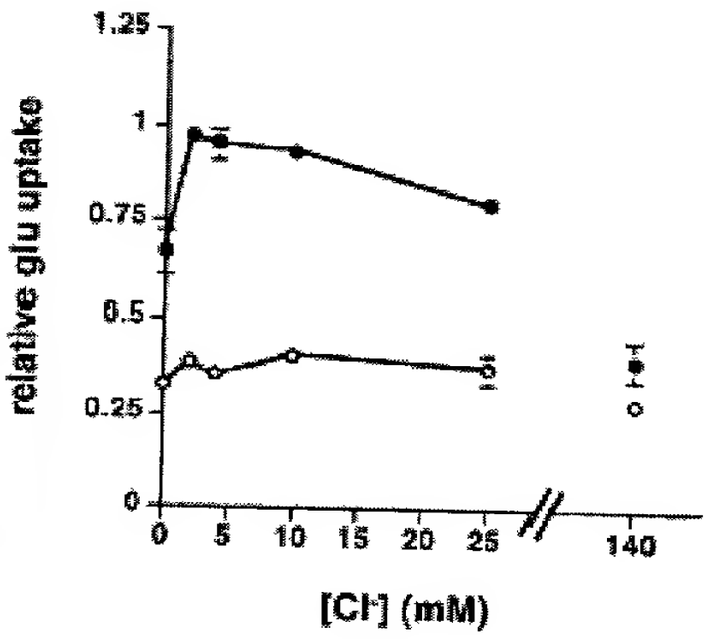


Fig. 13D

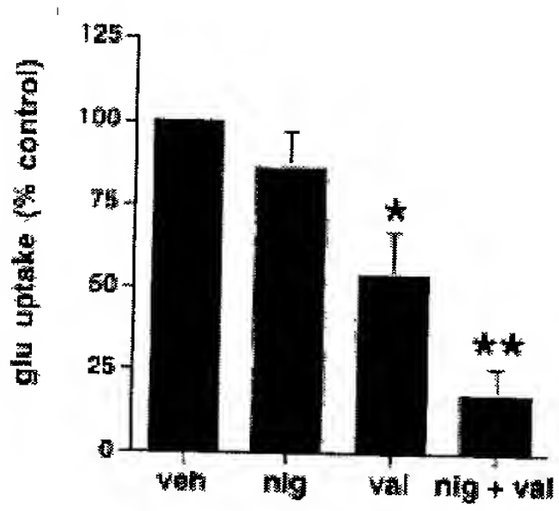


Fig. 13E